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Figure 1. DNA and Amino Acid Sequences of the Diversified Region of Subtilisin.

Amino acid sequence of pre-pro peptide shown in small letters. Amino acid sequence of the mature peptide are shown in capital letters. Amino acid sequence of the diversified region are shown in capital, bold letters.

m kkplgkivas
-100 tallisvafs ssiasaeea kekyligfne qeavsefv eq veandevail
-50 seeeeveiel lhefetipvl svelspedvd aleldpaisy ieedaevttm
1 AQSVPWGISR VQAPAAHNRG LTGSGVKAVV LDTGISTHPD LNIRGGASFV
51 PGE~~P~~**STQDGN GHGTHVAGTI AALNNSIGVL GVAPSAELYA VKVLGASGSG**
101 SVSSIAQGLE WAGNNGTHVA NLSLGSPSPS ATLEQAVNSA TSRGVLVAA
151 SGNSGAGGSIS YPARYANAMA VGATDQNNNR ASFSQYGAGL DIVAPGVNVQ
201 STYPGSTYAS LNGTSMATPH VAGVAALVKQ KNPSWSNVQI RNHLKNTATS
251 LGSTNLYGSG LVNAEAATR

2A

Subtilisin Structure-Function Correlation

Thermostability Motifs

Savineau, seq. G A S F V P 3 E P S T Q D O G N H G T H V A G T I A L N N S I G V L G V A P S A E L Y A V K V U L G A N G R G S Y S G I A C Q U L E 193

| Majority | STQDGNGHGTTHVAGTVAAALNNSIGVILGVAPSSADLYAVKVKVLGANGRGSYSGIAQULE | 76 |
|-----------|--|-----|
| 163, seq | - STQDGNGHGTTHVAGTVAAALNNSIGVILGVAPSSADLYAVKVKVLGANGRGSYSGIAQULE | 60 |
| 696, seq | - STQDGNGHGTTHVAGTVAAALNNSIGVILGVAPSSADLYAVKVKVLGANGRGSYSGIAQULE | 166 |
| 4C6, seq | - STQDGNGHGTTHVAGTVAAALNNSIGVILGVAPSSADLYAVKVKVLGANGRGSYSGIAQULE | 166 |
| 1b3, seq | - STQDGNGHGTTHVAGTVAAALNNSIGVILGVAPSSADLYAVKVKVLGANGRGSYSGIAQULE | 166 |
| 3e2, seq | - STQDGNGHGTTHVAGTVAAALNNSIGVILGVAPSSADLYAVKVKVLGANGRGSYSGIAQULE | 166 |
| 5h9, seq | - STQDGNGHGTTHVAGTVAAALNNSIGVILGVAPSSADLYAVKVKVLGANGRGSYSGIAQULE | 166 |
| 3a7, seq | - STQDGNGHGTTHVAGTVAAALNNSIGVILGVAPSSADLYAVKVKVLGANGRGSYSGIAQULE | 166 |
| 5h11, seq | - STQDGNGHGTTHVAGTVAAALNNSIGVILGVAPSSADLYAVKVKVLGANGRGSYSGIAQULE | 166 |
| 4d10, seq | - STQDGNGHGTTHVAGTVAAALNNSIGVILGVAPSSADLYAVKVKVLGANGRGSYSGIAQULE | 166 |
| 1f6, seq | - STQDGNGHGTTHVAGTVAAALNNSIGVILGVAPSSADLYAVKVKVLGANGRGSYSGIAQULE | 166 |
| 4C2, seq | - STQDGNGHGTTHVAGTVAAALNNSIGVILGVAPSSADLYAVKVKVLGANGRGSYSGIAQULE | 166 |

Savineau, seq. G A S F V P 3 E P S T Q D O G N H G T H V A G T I A L N N S I G V L G V A P S A E L Y A V K V U L G A N G R G S Y S G I A C Q U L E 193

| Majority | W A A A N M H I A N M S L G S D A P S T T L E R A V N Y A T S Q G V U V I A T G N G S - S V G Y P A R Y A N A M A V G A T D | 76 |
|-----------|---|-----|
| 1a1, seq | W A A A N M H I A N M S L G S D A P S T T L E R A V N Y A T S Q G V U V I A T G N G S - S V G Y P A R Y A N A M A V G A T D | 110 |
| 696, seq | W A A A N M H I A N M S L G S D A P S T T L E R A V N Y A T S Q G V U V I A T G N G S - S V G Y P A R Y A N A M A V G A T D | 110 |
| 4C6, seq | W A A A N M H I A N M S L G S D A P S T T L E R A V N Y A T S Q G V U V I A T G N G S - S V G Y P A R Y A N A M A V G A T D | 110 |
| 1b3, seq | W A A A N M H I A N M S L G S D A P S T T L E R A V N Y A T S Q G V U V I A T G N G S - S V G Y P A R Y A N A M A V G A T D | 110 |
| 3e2, seq | W A A A N M H I A N M S L G S D A P S T T L E R A V N Y A T S Q G V U V I A T G N G S - S V G Y P A R Y A N A M A V G A T D | 110 |
| 5h9, seq | W A A A N M H I A N M S L G S D A P S T T L E R A V N Y A T S Q G V U V I A T G N G S - S V G Y P A R Y A N A M A V G A T D | 110 |
| 3a7, seq | W A A A N M H I A N M S L G S D A P S T T L E R A V N Y A T S Q G V U V I A T G N G S - S V G Y P A R Y A N A M A V G A T D | 110 |
| 5h11, seq | W A A A N M H I A N M S L G S D A P S T T L E R A V N Y A T S Q G V U V I A T G N G S - S V G Y P A R Y A N A M A V G A T D | 110 |
| 4d10, seq | W A A A N M H I A N M S L G S D A P S T T L E R A V N Y A T S Q G V U V I A T G N G S - S V G Y P A R Y A N A M A V G A T D | 110 |
| 1f6, seq | W A A A N M H I A N M S L G S D A P S T T L E R A V N Y A T S Q G V U V I A T G N G S - S V G Y P A R Y A N A M A V G A T D | 110 |
| 4C2, seq | W A A A N M H I A N M S L G S D A P S T T L E R A V N Y A T S Q G V U V I A T G N G S - S V G Y P A R Y A N A M A V G A T D | 110 |

Savineau, seq. W A G V N O W H V A N L S L G S P S A T L E Q A V N S A T S R G V L V V A A S J H S G A S I S Y P A R Y A N A V G A T D 193

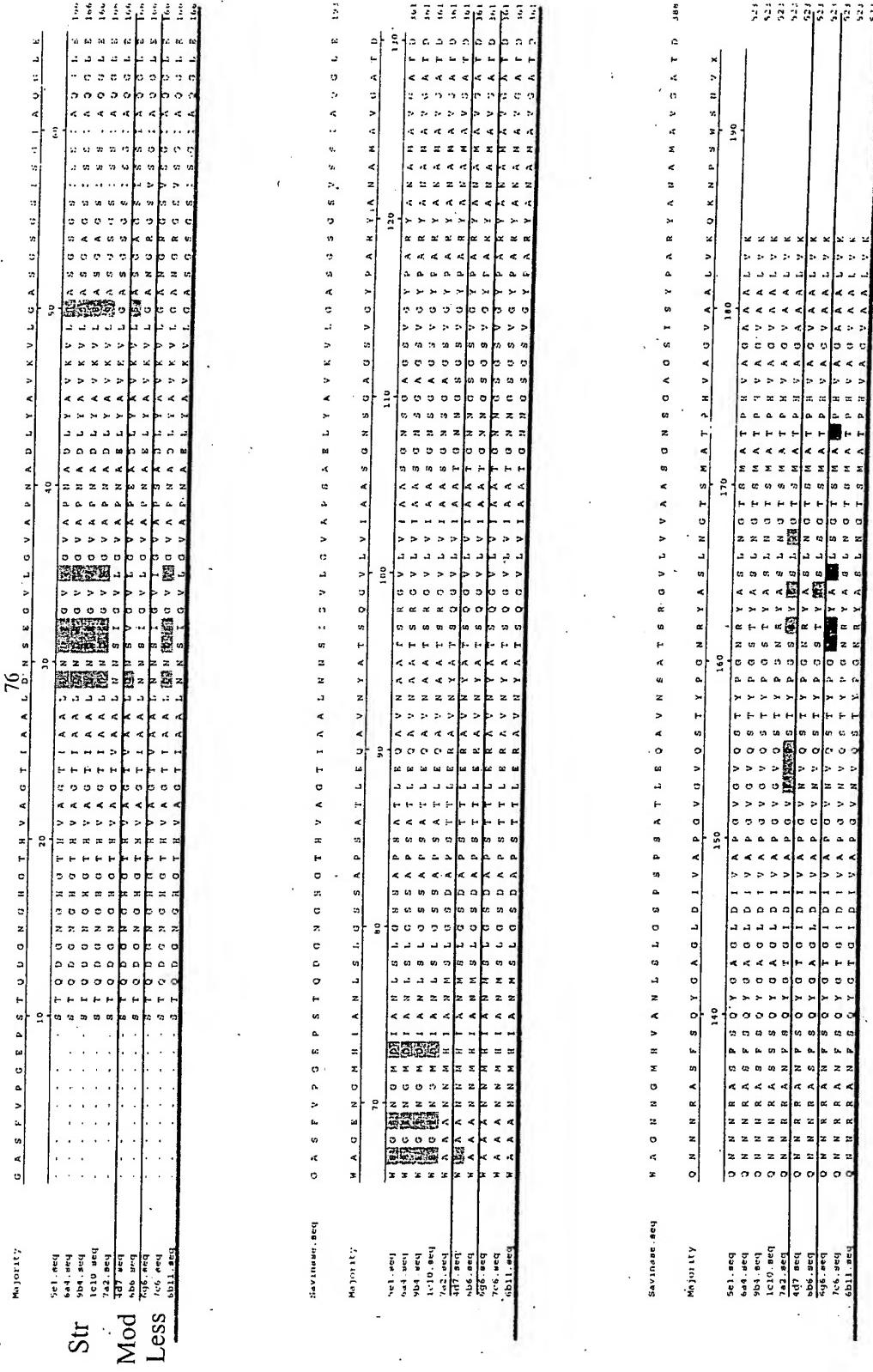
| Majority | Q N N R R A N F S O Y G T G I D I V A P G V N V Q S T Y P G N R Y A S L N G T S M A T P H U V A G A A A L V K | 76 |
|-----------|---|-----|
| 1a1, seq | Q N N R R A N F S O Y G T G I D I V A P G V N V Q S T Y P G N R Y A S L N G T S M A T P H U V A G A A A L V K | 190 |
| 696, seq | Q N N R R A N F S O Y G T G I D I V A P G V N V Q S T Y P G N R Y A S L N G T S M A T P H U V A G A A A L V K | 190 |
| 4C6, seq | Q N N R R A N F S O Y G T G I D I V A P G V N V Q S T Y P G N R Y A S L N G T S M A T P H U V A G A A A L V K | 190 |
| 1b3, seq | Q N N R R A N F S O Y G T G I D I V A P G V N V Q S T Y P G N R Y A S L N G T S M A T P H U V A G A A A L V K | 190 |
| 3e2, seq | Q N N R R A N F S O Y G T G I D I V A P G V N V Q S T Y P G N R Y A S L N G T S M A T P H U V A G A A A L V K | 190 |
| 5h9, seq | Q N N R R A N F S O Y G T G I D I V A P G V N V Q S T Y P G N R Y A S L N G T S M A T P H U V A G A A A L V K | 190 |
| 3a7, seq | Q N N R R A N F S O Y G T G I D I V A P G V N V Q S T Y P G N R Y A S L N G T S M A T P H U V A G A A A L V K | 190 |
| 5h11, seq | Q N N R R A N F S O Y G T G I D I V A P G V N V Q S T Y P G N R Y A S L N G T S M A T P H U V A G A A A L V K | 190 |
| 4d10, seq | Q N N R R A N F S O Y G T G I D I V A P G V N V Q S T Y P G N R Y A S L N G T S M A T P H U V A G A A A L V K | 190 |
| 1f6, seq | Q N N R R A N F S O Y G T G I D I V A P G V N V Q S T Y P G N R Y A S L N G T S M A T P H U V A G A A A L V K | 190 |
| 4C2, seq | Q N N R R A N F S O Y G T G I D I V A P G V N V Q S T Y P G N R Y A S L N G T S M A T P H U V A G A A A L V K | 190 |

Savineau, seq. Q N N R R A S P S Q Y G A Q ' D I V A P G V N V Q S T Y P G S T Y A S L N G T S M A T P H U V A G A A A L V K N P S W S S V X 590

2B

Subtilisin Structure-Function Correlation

pH Shifting Motifs



Sequence logos for pH shifting motifs across four subtilisins (Str, Mod, Less, Sav) at positions 76 and 120. The y-axis represents the position of the amino acid residue, and the x-axis represents the frequency of each amino acid (A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y) at that position.

20

Subtilisin Structure-Function Correlation Activity in DMF Motifs

There are many ways to do this, but one common approach is to use a *for* loop to iterate over the array and update each element.

| W A A A N M H I A N S L O S D A P S A T T L E Q A V N Y A T S K G V U L I A T O N G S S G Y P A R Y V A N A M A V A T | |
|---|------|
| 70 | 70 |
| 80 | 80 |
| 90 | 90 |
| 100 | 100 |
| 110 | 110 |
| 120 | 120 |
| 130 | 130 |
| 140 | 140 |
| 150 | 150 |
| 160 | 160 |
| 170 | 170 |
| 180 | 180 |
| 190 | 190 |
| 200 | 200 |
| 210 | 210 |
| 220 | 220 |
| 230 | 230 |
| 240 | 240 |
| 250 | 250 |
| 260 | 260 |
| 270 | 270 |
| 280 | 280 |
| 290 | 290 |
| 300 | 300 |
| 310 | 310 |
| 320 | 320 |
| 330 | 330 |
| 340 | 340 |
| 350 | 350 |
| 360 | 360 |
| 370 | 370 |
| 380 | 380 |
| 390 | 390 |
| 400 | 400 |
| 410 | 410 |
| 420 | 420 |
| 430 | 430 |
| 440 | 440 |
| 450 | 450 |
| 460 | 460 |
| 470 | 470 |
| 480 | 480 |
| 490 | 490 |
| 500 | 500 |
| 510 | 510 |
| 520 | 520 |
| 530 | 530 |
| 540 | 540 |
| 550 | 550 |
| 560 | 560 |
| 570 | 570 |
| 580 | 580 |
| 590 | 590 |
| 600 | 600 |
| 610 | 610 |
| 620 | 620 |
| 630 | 630 |
| 640 | 640 |
| 650 | 650 |
| 660 | 660 |
| 670 | 670 |
| 680 | 680 |
| 690 | 690 |
| 700 | 700 |
| 710 | 710 |
| 720 | 720 |
| 730 | 730 |
| 740 | 740 |
| 750 | 750 |
| 760 | 760 |
| 770 | 770 |
| 780 | 780 |
| 790 | 790 |
| 800 | 800 |
| 810 | 810 |
| 820 | 820 |
| 830 | 830 |
| 840 | 840 |
| 850 | 850 |
| 860 | 860 |
| 870 | 870 |
| 880 | 880 |
| 890 | 890 |
| 900 | 900 |
| 910 | 910 |
| 920 | 920 |
| 930 | 930 |
| 940 | 940 |
| 950 | 950 |
| 960 | 960 |
| 970 | 970 |
| 980 | 980 |
| 990 | 990 |
| 1000 | 1000 |

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He was a man of great energy and determination, and he left a lasting legacy in the field of education.